

Amendment to the Specification

1. Please amend line 26 of page 38 to line 6 of page 39 of the specification as follows:

-- The data obtained by the sequence analysis were firstly processed using the Molecular BioComputing Suite (Muller *et al.*, 2001) and Sequences 3.0 programs, and the deduced protein sequences were determined. The BLAST (Altschul *et al.*, 1990) and omniBLAST programs were used for the database searches, that is the comparison with already known sequences in the EMBL and SwissProt databases or with the *Eimeria tenella* genome project data (~~www.sanger.ac.uk/Projects/E-tenella/~~). Two or more DNA or protein sequences were aligned using the BLAST 2 sequences (~~www.ncbi.nlm.nih.gov~~) (Tatusova and Madden, 1999), CLUSTALW (~~www.ebi.ac.uk~~) (Thompson *et al.*, 1994) and DIALIGN (Morgenstern *et al.*, 1998; 1999) programs. In addition, the SignalP (~~www.cbs.dtu.dk/services/SignalP/~~) (Nielsen *et al.*, 1997) and Clone Manager 5 programs were used for identifying signal peptides and, respectively, planning clonings and restrictions and for searching for open reading frames.--

Clean Version of the above paragraph:

-- The data obtained by the sequence analysis were firstly processed using the Molecular BioComputing Suite (Muller *et al.*, 2001) and Sequences 3.0 programs, and the deduced protein sequences were determined. The BLAST (Altschul *et al.*, 1990) and omniBLAST programs were used for the database searches, that is the comparison with already known sequences in the EMBL and SwissProt databases or with the *Eimeria tenella* genome project data. Two or more DNA or protein sequences were aligned using the BLAST 2 sequences (Tatusova and Madden, 1999), CLUSTALW (Thompson *et al.*, 1994) and DIALIGN (Morgenstern *et al.*, 1998; 1999) programs. In addition, the SignalP (Nielsen *et al.*, 1997) and Clone Manager 5 programs were used for identifying signal peptides and, respectively, planning clonings and restrictions and for searching for open reading frames.--

2. Please amend the table at line 17 of page 34 of the specification as follows:

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Primer (RT-PCR)	Sequence (5'-3') <u>SEQ ID NO</u>
A17-22-up	TCCTCATCCTTATCATCCTCATCCT <u>SEQ ID NO. 4</u>
A17-112-lo	GTGGGGATGATGGTGGG <u>SEQ ID NO. 5</u>
A17-f-length-64-up	CAGGACCCCAAAATAAAATCAAAGGCTATCACA <u>SEQ ID NO. 6</u>
A17-f-length-1176-lo	TGACCGGTGGTGTGTACTTCGTAAC <u>SEQ ID NO. 7</u>
<i>Et</i> ACTIN-up	CTGTGAGAAGAACCGGGTGCTCTTC <u>SEQ ID NO. 8</u>
<i>Et</i> ACTIN-lo	CGTGCGAAAATGCCGGACGAAGAG <u>SEQ ID NO. 9</u>

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Clean Version of the above table:

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Primer (RT-PCR)	SEQ ID NO
A17-22-up	SEQ ID NO. 4
A17-112-lo	SEQ ID NO. 5
A17-f-length-64-up	SEQ ID NO. 6
A17-f-length-1176-lo	SEQ ID NO. 7
<i>Et</i> ACTIN-up	SEQ ID NO. 8
<i>Et</i> ACTIN-lo	SEQ ID NO. 9

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3. Please amend the table at line 1 of page 35 of the specification as follows:

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Primer (RACE-PCR)	Sequence (5'-3') <u>SEQ ID NO</u>
A17-22-up	TCCTCATCCTTATCATCCTCATCCT <u>SEQ ID NO. 4</u>
A17-max-90-up	TGAGGACTATCCTAGCCACCCTAGTCCGTTTC <u>SEQ ID NO. 10</u>

A17-max-150-up	GAGCAGCTGAGTATCCTTCTCAGCTTGCAGTT <u>SEQ ID NO. 11</u>
A17-112-lo	GTGGGGATGATGGTGGG <u>SEQ ID NO. 5</u>
A17-max-533-lo	TATGTTTCATGATGATGATGGTGAGGATGATGG <u>SEQ ID NO. 12</u>
A17-max-631-lo	AGGATGCGCAAAATGGTAGTCATGGTGATAAT <u>SEQ ID NO. 13</u>

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Clean Version of the above table:

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Primer (RACE-PCR)	SEQ ID NO
A17-22-up	SEQ ID NO. 4
A17-max-90-up	SEQ ID NO. 10
A17-max-150-up	SEQ ID NO. 11
A17-112-lo	SEQ ID NO. 5
A17-max-533-lo	SEQ ID NO. 12
A17-max-631-lo	SEQ ID NO. 13

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4. Please amend the table at line 16 of page 37 of the specification as follows:

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5'-IRD-800 primer	Sequence (5'-3') <u>SEQ ID NO</u>
pG8SAET-up	TAGGTGTAGGTATTGCATCTGTAAGTT <u>SEQ ID NO. 14</u>
pG8SAET-lo	CGATATATTGGTGGCTGAGGCTTGGA <u>SEQ ID NO. 15</u>
pG8SAET-seq-up-140	ATGATGACTTTACAAATACATACAGGG <u>SEQ ID NO. 16</u>
A17-sequit-27-up	CGAGGAAGAGCAGCTTACCGACATCAACTAAG <u>SEQ ID NO. 17</u>

A17-sequit-44-up	CCGACATCAACTAAGCTATTGGTGGGGAATTA <u>SEQ ID NO. 18</u>
A17-sequit-385-lo	ATGAGGATAATTTGGCTGAGGATGCGGATAAT <u>SEQ ID NO. 19</u>
A17-sequit-351-lo	GGATGAGGATGGAGGTGAAAGTGGTAAGTTGT <u>SEQ ID NO. 20</u>
M13 reverse	CGAGAAACAGCTATGAC <u>SEQ ID NO. 21</u>
M13 forward	GTAAAACGACGGCCAG <u>SEQ ID NO. 22</u>
T7-Promotor	ATTATGCTGAGTGATATCCC <u>SEQ ID NO. 23</u>
BGH reverse	TAGAAGGCACAGTCGAGG <u>SEQ ID NO. 24</u>

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Clean Version of the above table:

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5'-IRD-800 primer	SEQ ID NO
pG8SAET-up	SEQ ID NO. 14
pG8SAET-lo	SEQ ID NO. 15
pG8SAET-seq-up-140	SEQ ID NO. 16
A17-sequit-27-up	SEQ ID NO. 17
A17-sequit-44-up	SEQ ID NO. 18
A17-sequit-385-lo	SEQ ID NO. 19
A17-sequit-351-lo	SEQ ID NO. 20
M13 reverse	SEQ ID NO. 21
M13 forward	SEQ ID NO. 22
T7-Promotor	SEQ ID NO. 23
BGH reverse	SEQ ID NO. 24